



SEQUENCE LISTING

<110> GONG, ZHIYUAN  
HE, JIANGYAN  
JU, BENSHENG  
LAM, TOONG JIN  
XU, YANFEI  
YAN, TIE

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT  
TRANSGENIC ORNAMENTAL FISH

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<140> 10/605,708

<141> 2003-10-21

<150> 09/913,898

<151> 2001-10-03

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Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser	
145 150 155	
gac gtt cag ctt atc aaa cct gga gac aag gtg ggc gcc agc gag gcc	590
Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala	
160 165 170	
acg ctg ctg aac atg ctg aac atg ctg aac atc tcc ccc ttc tcc tac	638
Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr	
175 180 185	
ggg ctg atc atc cag cag gtg tat gat aac ggc agt gtc tac agc ccc	686
Gly Leu Ile Ile Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro	
190 195 200	
gag gtg ctg gac atc act gag gac gcc ctg cac aag agg ttc ctg aag	734
Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys	
205 210 215 220	
ggt gtg agg aac atc gcc agt gtg tgt ctg cag atc ggc tac cca act	782
Gly Val Arg Asn Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr	
225 230 235	
ctt gct tcc atc cct cac act atc atc aat gga tac aag agg gtc ctg	830
Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu	
240 245 250	
gct gtc act gtc gaa aca gac tac aca ttc ccc ttg gct gag aag gtg	878
Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val	
255 260 265	
aag gcc tac ctg gct gat ccc acc gct ttc gct gtt gca gcc cct gtt	926

Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val  
 270 275 280

gcg gca gct aca gag cag aaa tcc gct gct cct gcg gct aaa gag gag 974  
 Ala Ala Ala Thr Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu  
 285 290 295 300

gca ccc aag gag gat tct gag gag tct gat gaa gac atg ggc ttc ggc 1022  
 Ala Pro Lys Glu Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly  
 305 310 315

ctg ttt gat taa accagacacc gaatatccat gtctgttttaa catcaataaa 1074  
 Leu Phe Asp  
 320

acatctggaa aaaaaaaaaa aaaaaaaaaa 1104

<210> 6  
 <211> 319  
 <212> PRT  
 <213> Danio rerio

<400> 6  
 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys  
 1 5 10 15  
 Ile Ile Gln Leu Asp Asp Phe Pro Lys Cys Phe Ile Val Gly Ala  
 20 25 30  
 Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg Leu Ser Leu Arg  
 35 40 45  
 Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala  
 50 55 60  
 Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro  
 65 70 75 80  
 His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr  
 85 90 95  
 Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg  
 100 105 110  
 Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr  
 115 120 125  
 Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr  
 130 135 140  
 Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu  
 145 150 155 160  
 Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn  
 165 170 175  
 Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile  
 180 185 190  
 Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp  
 195 200 205  
 Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn  
 210 215 220  
 Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile  
 225 230 235 240  
 Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val  
 245 250 255  
 Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu

	260		265		270										
Ala	Asp	Pro	Thr	Ala	Phe	Ala	Val	Ala	Ala	Pro	Val	Ala	Ala	Ala	Thr
	275						280				285				
Glu	Gln	Lys	Ser	Ala	Ala	Pro	Ala	Ala	Lys	Glu	Glu	Ala	Pro	Lys	Glu
	290						295				300				
Asp	Ser	Glu	Glu	Ser	Asp	Glu	Asp	Met	Gly	Phe	Gly	Leu	Phe	Asp	
305					310				315						

<210> 7  
 <211> 2241  
 <212> DNA  
 <213> Danio rerio

<220>  
 <221> TATA signal  
 <222> (2103)..(2108)

<220>  
 <221> primer bind  
 <222> (2221)\_(2241)  
 <223> CK2

<220>  
 <221> misc feature  
 <222> (2142)..(2235)  
 <223> Identical to the 5' CK cDNA

<400> 7  
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 tcacacctgg tttatactat gatagttgta cagtgtctggc tgtgacaccc aactgtctgcc 120  
 aattgtctga ctatgcaggg tgtctatgcg tatagtttac agttagacca aagtgtgctg 180  
 gtgtgtgaag taacaaatga caaatactca aattgtaatt tactaagtag tttaaaaatg 240  
 tagtgcagtg ttggtacttt tatttcactt ttattcttgt ctatgtggat tagacaaatc 300  
 acatagaagg taaatcacat cataatgaac agcaaactgt ttgccagcat taaaagaaga 360  
 agactgctta gatgcatgtc actgatgaga aaataacttt aaacgcacac aagacggcac 420  
 gtacccaac gcagtgggga cgttgcattt gaactcaacg tcaggtcgat gtcaatgttc 480  
 ctaatgatgt tacagcttga tgttatgcgg ggattatggg tgccatacct gatgaataaa 540  
 ggttcgacat tggattttgg tcgctttcca cctatgacat cgttattgga cgtcaaaata 600  
 aatttaggtc accacaacct atatttaacc tgctgggcaa taactaaatg cactacagaa 660  
 taaatgcac agcttttcac agcataatac aaaagctact tttcactcat actttgagta 720  
 acatttttag gcatgtattg atatttttac cagccctccc catacataat cgtatgttta 780  
 acattagctt tgtagccgc tagcattact gagcttgtgc atgaaagcag atttggagct 840  
 gatgattgcc gtaccatgat ctcacacctt gacgattgcg taatgctatt aaatgcccat 900  
 atttcgtgtt gacttgcacg agaaatgaga tgggaacatt tatcagtggg cattaaatac 960  
 tatttttgtg ttagcttagc tgcagttttt aactattgta attaatagat ttttctcaga 1020  
 tgtactttta ctttccttg agtacatttt ccttccttca acctgcagtc actactttat 1080  
 agtcctgtga ttctgtcca atcaaattgc taccttaaga catggggccat ttataattgc 1140  
 tgtcaaaaat atttacacgc attaaccag agatgatgga tgtttactgt atgatgaccg 1200  
 aagacgtcaa catggcggtta ggttgacgtt tgtttagaaa tgaaaattag gttgacgtca 1260  
 aacatccaat ctaaaatcat atatcaatgt atgttaccct tatgacgtct atcagacgtt 1320  
 tgtcattatt tgacgttggg ttaagatgtt acacaacct aatccaccaa atattaactt 1380  
 acaatatcct tagatgctgg ctgactttg taatattaac atcttatgat gttgtgtgcc 1440  
 tgttacgttt acacacatgt aaattacatg tcactactta ctactcttga gtacttttaa 1500  
 atatttacia ctgatacttt tactcgcact tatgattttt cagtactctt tccactactg 1560  
 cacatatggg ggagtttaga gccataatct gtgcagaatt gtgtgtgtgc acattttcca 1620  
 atatcaatac agaaggaaac tgtgttcctt gttcccttgt aaatctcaac aatgcaactg 1680

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ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaaaag tgaatggaaa 1740
aaagcctttc attaatgtga aagttgctgc gcgccccacc cagataaaaa gagcagaggt 1800
taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca cccccgctgg 1860
cagatgggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtcctcaagt 1920
ctcaagcctc tccttgcatc ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
caacatttat cttaccactt tctctctgta cctgtctaac aggtagggtg tgtgtgagag 2040
tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtca gctccaccct ctcaagagtg 2100
tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
tgagcaacct cctccactca ctctctctc agagagcact ctcgtacctc cttctcagca 2220
actcaaagac acaggatccg g                                     2241

```

```

<210> 8
<211> 1456
<212> DNA
<213> Danio rerio

```

```

<220>
<221> TATA signal
<222> (1389)..(1394)

```

```

<220>
<221> primer bind
<222> (1433)_(1456)
<223> MCK2

```

```

<220>
<221> misc feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA

```

```

<400> 8
gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
tgtggcttaa tcttggctga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
gcatgtgcac catgacaggc ctgttattca cacttgggtg catgttggag actgttcggc 180
cagctatagt tttcttcaca gagtccctggg tcacctaatg tcacaaggaa gaaacatgtt 240
acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
ttacagctta aaagattgct agacagaaaa accagggagg ggttttccca taatatccag 360
tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
gtgacagaaa accagagatg gaaataacct cttttgaatt gcataattgc ttaaaagaag 480
acacaacagg gatagttcac ccaaaaaaca gaccattctt tttttctgtt gaacaaaaat 540
taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
aagtcaatgg gtcttccagc attttttcaa tataccttac tttgagttca aaagaaaaac 660
acatctcaaa taggtttgag gttgaataaa catttttcat tttggggtgg actatcccta 720
attatttgac acttaagatt tatagtaaat cattttatag acttttctccc cttattaaac 780
atggttgaat ttatcttcat gtttatgtct gggttgtgct tttttgaaaa gatttccctg 840
tcaaattgtt ttgtgtatgg ttggcgca caatagactgaa ctggcctatc acacagactt 900
tcataacaac tccagttgat gccctttcac cctcagtgta taaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaaatt gagtttgacac 1020
ccagaatcat gtggtgaacg aagcctacca agagattttt gaaagccatc ggcctgacac 1080
gcgcacttct gatatctgtg gtatgttttg caaaagtgtc gctcagcctt tttagcatgg 1140
cagatcctcc acatcccac acccctcctt caacctatc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccaca gctgccacct 1260
catctaggat gcctggggcc taaattgaag cctttcttac actaaacagg gcataagaga 1320
ccagcgccag ccaatcataa ttcagtgcgc tctaaaatgg gccagccaat ggctgcaggg 1380
gctagaggta tatatatcca aatcaaactc ttcttgcttg ggtgaccctt atttcggctt 1440
ggtgaacagg atccgg                                     1456

```

<210> 9  
<211> 2205  
<212> DNA  
<213> Danio rerio

<220>  
<221> primer bind  
<222> (2179)..(2205)  
<223> ARP2

<220>  
<221> misc\_feature  
<222> (2153)..(2199)  
<223> Identical to the 5' ARP cDNA

<220>  
<221> intron  
<222> (792)..(2152)

<220>  
<221> misc\_feature  
<222> (775)..(791)  
<223> Identical to the 5' ARP cDNA

<400> 9  
atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgatc 60  
atTTtaattt gtgttgata attttacatt ttgtaagtat tatttttata aaaaatatat 120  
agaaataata caaatttggt tacagtattc ttagttattg caataaacga attttatata 180  
gaaagagaaa gagttttatt ataagatgtt caatttataaa aatggcagaa aatagaaaaa 240  
tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300  
agataataaa gtgacttttt tgggcggacc aaatttccct attaatgggtc aattcattaa 360  
aatacattca ttaaaataaa ggtattgcca tgaatttaga tgcacagtga ttttggttct 420  
gtgcagattt ttggctgttg ttagaaggga tacatctgcg gccgaaagt aacgggaact 480  
atttacattc tttgctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540  
tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaatgatgc 600  
tatattgacc gcagctgtat cctttctaag tgcgactgta caaatacgca ctgaccgtga 660  
cagacacgtg cattgaccaa tcagcgcaca gatacgcat ttccgcgcga ttctgattgg 720  
atgatcgact gatactaata ttgtgccgct tcctttcgcg gcctctttct ttcacgcgtc 780  
cctaccgtga ggtaaggctg acgccgctct tgtggcgggt tcttaaaatg tgtaataaaa 840  
taacatcata agaggtcacg agaaggctca cgtgtgttta atatcagcgg cggttattat 900  
tatgcgttta aagcttgtgt aatgattttt acagtaaaag ttagcactag cctgttagca 960  
caggcctcgt gcgccatgtg tgacgcgacg ttttaatagc atcttatttg attttgatga 1020  
tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080  
ttacatgcta gtacttgtgc tagtcggtcg atccacattg agatgttgcg ctatttgcca 1140  
ttttaaacc agttactctc attttagtga aatattctta agccactaag ttaaaatttg 1200  
tcaatcacat ataattgtgt ttatgtttta tttgagtcat cataccagg aatagtttta 1260  
tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320  
gtaaaggtaa tcttaagggt gtaaaggctc acccaaaaaga caattcaccg tcaagtgttt 1380  
tcaaacttta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440  
accataatac aaatacagga aaaatatact atagaagtgc atggttacag gttttctgca 1500  
ttcaaaatat ctacacaagt gttaaatgga aggaactcaa gtgatttgaa aagttaaggg 1560  
tgcataaatc agttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620  
gcagtggcca ccaagcttgt tcctgaaggg ccagtgtcct acagatttta gctccaaccc 1680  
taattaaaca cacctgaaca agctaataca ggtcttacta ggtatgtttg aaacatccag 1740  
gcagggtgtg tgatgcaaga tagagctaaa ccctgcaggg acaatggccc aacaggattg 1800  
gtgaccctg cctcaagcca tcacaaatgc attatggtat taagaaatgt gcaggttcag 1860

ttatggacag gctgttgacg tgcttggtcg tcgttccac tgcacaaatg aacatgattc 1920  
 cttctatccc tgtctgtctg catctcatga cttgcagga cgctggtctc agacacgttt 1980  
 atagcagtaa atcaaataca atagtgtctt gattatcttt aaatatttga aagcttataa 2040  
 taggcaacca aattacctgg aaacagttta caaacagtaa ttcataattt gtcatttaaat 2100  
 aagatgcaca caaggcagggt gtaaaagtat tgcttggtgt tgtaatcctc agattttaca 2160  
 accttgctct taaaccggct gttcacgat ccttggaagg gatcc 2205

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytokeratin - gene specific primer

<400> 10

cgctggagta agagatagac ctgg

24

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytokeratin gene specific primer

<220>

<221> misc feature

<222> (1)..(6)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (3)..(8)

<223> BamHI site

<400> 11

cggatcctg tgtctttgag ttgctg

26

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Muscle creatine kinase gene specific primer

<220>

<221> misc feature

<222> (3)..(8)

<223> BamHI site

<400> 12

ccggatcctt gggatcagat cctg

24

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Muscle creatine kinase gene specific primer

<220>

<221> misc feature

<222> (1)..(3)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (3)..(B)

<223> BamHI site

<400> 13

ccggatcctg ttcaccaagc cgaa

24

<210> 14

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Acidic ribosomal protein PO gene specific primer

<400> 14

tagttggact tccacgtgcc ctgtc

25

<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Acidic ribosomal protein PO gene specific primer

<220>

<221> misc feature

<222> (1)..(7)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (1)..(6)

<223> BamHI site



<400> 15  
ggatcccttc caaggatcgg tgaaca 26

<210> 16  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide for linker used in linker-mediated PCR

<400> 16  
gttcatcttt acaagctagc gctgaacaat gctgtggaca agcttgaatt c 51

<210> 17  
<211> 10  
<212> DNA  
<213> Artificial Sequence

<223> Description of Artificial Sequence:  
Oligonucleotide for linker used in linker-mediated PCR

<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> n is a dideoxycytidine

<400> 17  
gaattcaagn 10

<210> 18  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
linker specific primer

<400> 18  
gttcatcttt acaagctagc g 21

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
linker specific primer

<400> 19  
tcctgaacaa tgctgtggac

20

<210> 20  
<211> 1392  
<212> DNA  
<213> Danio rerio

<220>  
<221> CDS  
<222> (42)..(551)

<220>  
<221> primer bind  
<222> (6)..(28)  
<223> M2

<220>  
<221> primer bind  
<222> (23)..(45)  
<223> M1

<220>  
<221> polyA signal  
<222> (797)..(802)

<220>  
<221> polyA\_signal <222> (1351)..(1357)

<400> 20  
ctcttcttga tcttcttaga cttcacacat accgtctcga c atg gca ccc aag aag 56  
Met Ala Pro Lys Lys  
1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104  
Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser  
10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152  
Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile  
25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200  
Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp  
40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248  
Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu  
55 60 65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296  
Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu  
70 75 80 85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344  
Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile

90	95	100	
gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag			392
Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys			
105	110	115	
aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc			440
Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr			
120	125	130	
gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct			488
Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala			
135	140	145	
ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag			536
Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu			
150	155	160	165
gag aag gag gag taa acaaccttgg aatagaggaa acgaagagaa gaacatgcat			591
Glu Lys Glu Glu			
170			
cctcacagct taatctccag tctgttgtct ggccttctct aacttttgtt tttccttcct			651
ccctttcttg ctttctacca tcgttggttac tccaagcact tacactctcc atcttaccaa			711
agacttgtct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt			771
cgagtgggga catgggattg ttttcaataa aatgaacatc atttctgtat ctctcacatt			831
ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag			891
cttgcattgta agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta			951
tagtttgggg ctgaaacatc tctctagatc aatgtggaag agtgctcact ctgaggggga			1011
aagaagcacg atggagtgat ctcaacttat aatagaggaa ccagtcatca ttctcatttc			1071
ctcctctggg ggttgactaa aaagagaaaag agaaaatgag ggttttgtgc tgagtgagtt			1131
tagcctccta aaagcgatgc cgagctcatc acagagggag tgagagggac agaccatcct			1191
aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctcccct			1251
cctcttctct atttctctgt ccattctttc ttttttcttt tttctttttt gctttctgca			1311
tctgggcctg ctttgctctg ccaaacctct cctgtaacca ataaaaagac acaaactgtg			1371
aataaaaaaa aaaaaaaaaa a			1392

<210> 21  
 <211> 169  
 <212> PRT  
 <213> Danio rerio

<400> 21  
Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser  
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Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys  
20 25 30  
Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys  
35 40 45  
Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys  
50 55 60  
Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn  
65 70 75 80  
Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp  
85 90 95  
Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly  
100 105 110  
Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln  
115 120 125  
Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe  
130 135 140  
Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val  
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